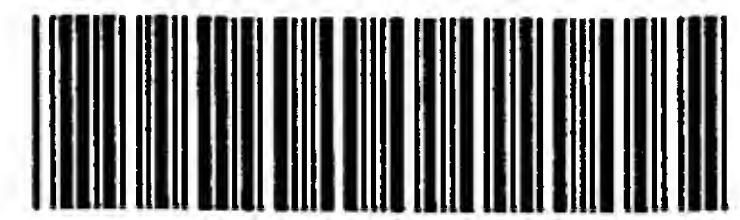


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/569,959
Source: IFW0
Date Processed by STIC: 11/30/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/569,959

DATE: 11/30/2006

TIME: 13:29:16

Input Set : N:\efs\11_30_06\10569959_efs\pto.da.txt
 Output Set: N:\CRF4\11302006\J569959.raw

3 <110> APPLICANT: Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo
 5 <120> TITLE OF INVENTION: Cyclic maltosylmaltose, cyclic maltosylmaltose-forming
 enzyme, their
 6 preparation and uses
 8 <130> FILE REFERENCE: 10102802
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/569,959
 C--> 10 <141> CURRENT FILING DATE: 2006-02-28
 10 <160> NUMBER OF SEQ ID NOS: 10
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 5
 14 <212> TYPE: PRT
 15 <213> ORGANISM: Arthrobacter globiformis
 17 <400> SEQUENCE: 1
 18 Asp Pro Thr Thr Ser
 19 1 5
 21 <210> SEQ ID NO: 2
 22 <211> LENGTH: 583
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Arthrobacter globiformis
 26 <400> SEQUENCE: 2
 27 Asp Pro Thr Thr Ser Pro Gly Pro Leu Ala Glu Gly Asp Val Ile Tyr
 28 1 5 10 15
 29 Gln Val Leu Val Asp Arg Phe Glu Asp Gly Asp Pro Thr Asn Asn Asp
 30 20 25 30
 31 Gln Gly Asp Gly Glu Tyr Asp Pro Ser Asp Leu Gly Phe Tyr His Gly
 32 35 40 45
 33 Gly Asp Trp Ala Gly Leu Thr Asp Arg Leu Asp Tyr Ile Ala Asp Leu
 34 50 55 60
 35 Gly Val Thr Ala Ile Trp Leu Ser Pro Val Ser Glu Gln Gln Pro Leu
 36 65 70 75 80
 37 Ser Arg Asp Gly Leu Glu Ala Ser Tyr His Gly Tyr Phe Thr Arg Asp
 38 85 90 95
 39 Phe Ala Thr Pro Asn Glu His Phe Gly Asp Arg Ala Glu Leu Gln Glu
 40 100 105 110
 41 Leu Ile Asp Thr Ala His Asp Leu Gly Leu Lys Met Ile Leu Asp Val
 42 115 120 125
 43 Val Pro Asn His Thr Ala Asp Tyr Leu Ala Gly Thr Ser Thr Thr Tyr
 44 130 135 140
 45 Ser Pro Ser Thr Tyr Lys Pro Ala Ser Pro Leu Asp Asp Ala Ser Tyr
 46 145 150 155 160
 47 Phe His His Ala Gly Asp Cys Leu Phe Asn Gly Leu Glu Thr Gln Thr
 48 165 170 175
 49 Gln Ile Glu Asn Cys Asp Leu Gly Gly Leu Asp Asp Leu Asp Gln Ser
 50 180 185 190

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Output Set: N:\CRF4\11302006\J569959.raw

51 Asn Pro Val Val Ser Ser His Leu Met Ser Thr Tyr Lys Asp Trp Val
52 195 200 205
53 Asp Met Gly Phe Asp Gly Ile Arg Val Asp Ala Ala Arg Ser Val Pro
54 210 215 220
55 Lys Pro Trp Leu Ala Asp Phe Glu Ala Glu Met Gly Val Pro Thr Phe
56 225 230 235 240
57 Gly Glu Val Phe Val Gly Asp Val Asp Tyr Val Ser Glu Tyr Gln Asp
58 245 250 255
59 Tyr Glu Trp Gly Val Leu Asp Phe Pro Tyr Phe Phe Thr Val Arg Glu
60 260 265 270
61 Ala Phe Ser Ala Asp Thr Asp Met Asn Lys Leu Gly Asp Leu Phe Asp
62 275 280 285
63 Gln Asp Ser Lys Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp
64 290 295 300
65 Asn His Asp Arg Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln
66 305 310 315 320
67 Arg Leu Arg Ser Gly Leu Thr Phe Leu Leu Thr Ser Arg Gly Val Pro
68 325 330 335
69 Val Ile Tyr Tyr Gly Thr Glu Gln Ala Asp Asp Gly Asn Gly Asn Pro
70 340 345 350
71 Tyr Glu Val Pro Ile Ala Asn Lys Asp Asn Arg Lys Asp Met Glu Ser
72 355 360 365
73 Phe Asp Gln Asn Ser Asn Leu Tyr Lys His Ile Gln Arg Leu Thr Ala
74 370 375 380
75 Ile Lys Ala Ala Tyr Pro Ala Leu Gln Val Gly Thr Gln Arg Glu Met
76 385 390 395 400
77 Trp Ser Asp Thr Ser Val Tyr Gly Phe Ser Arg Arg Val Asp Ser Thr
78 405 410 415
79 Gly Ala Glu Ala Met Thr Phe Ser Ser Asn Ser Trp Thr Thr Gln Thr
80 420 425 430
81 Arg Thr Val Pro Leu Arg Ala Glu Ser Ser Ile Thr Val Gly Thr Thr
82 435 440 445
83 Leu Thr Asn Leu Met Asn Thr Gly Asp Thr Val Thr Val Thr Ala Gly
84 450 455 460
85 Gly Val Thr Gly Lys Gln Ile Thr Val Ser Leu Gly Glu His Glu Ser
86 465 470 475 480
87 Lys Val Tyr Ala Pro Gly Thr Pro Val Ser Ala Tyr Ser Pro Glu Ala
88 485 490 495
89 Arg Asn Thr Thr Lys Ile Arg Val His Tyr Asn Val Gly Leu Gly His
90 500 505 510
91 Ser Ile Ala Ile Arg Gly Asp Glu Tyr Pro Phe Thr Trp Thr Ser Gly
92 515 520 525
93 Arg Gly Ala Arg Asn Val Ala Ser Asp Val Trp Glu Phe Glu Val Glu
94 530 535 540
95 Arg Ile Pro Asp Gly Glu Thr Phe Gln Phe Lys Pro Leu Ile Asp Asp
96 545 550 555 560
97 Val Thr Trp Ser Thr Gly Gly Asn Phe Thr Gly Thr Gly Gly Asp Val
98 565 570 575
99 Ile Asp Ile Tyr Pro Thr Phe

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Input Set : N:\efs\11_30_06\10569959_efs\pto.da.txt
Output Set: N:\CRF4\11302006\J569959.raw

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 103 <211> LENGTH: 1749
 104 <212> TYPE: DNA
 105 <213> ORGANISM: Arthrobacter globiformis
 107 <400> SEQUENCE: 3
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 109 gaccgggtcg aagacggcga ccccaccaac aacgaccagg ggcacggaga gtacgatccg 120
 110 tccgacctcg gtttctacca cggcggcgac tgggcgggccc tgacggaccg gctcgactac 180
 111 atcgccgatc tgggtgtgac ggcgatctgg ctctcgcccc tctccgagca gcagccgctc 240
 112 tcgcgcgacg ggctggaggc cagctaccac ggctacttca ctcgggactt cgccgacgccc 300
 113 aacgagcatt tcggcgaccc agccgagctg caggagctga tcgacacggc gcacgatctc 360
 114 ggactcaaga tgcgttacca cgtcgtgccc aaccacacgg ccgactaccc cgccggcaca 420
 115 tcgacgaccc attcgccgag cacctacaag ccggcgagtc cgctcgatga cgctcgat 480
 116 ttccatcactg ccggcgactg cctgttcaac gggctcgaga cgccggccca gatcgagaac 540
 117 tgcgacctcg gcgggctcga cgacctcgat cagtcgaacc cggtcgatcg tgcgcaccc 600
 118 atgagcacgt acaaggactg ggtcgacatg ggcttcgacg gcatccgggt cgatcgccg 660
 119 cgctcggtgc cgaagccgtg gctcgccgac ttcaagccg agatggcgat gcccaccc 720
 120 ggcgagggtgt tgcgttacca tgcgttaccc gtctcgatcc accaggacta cgagtggggc 780
 121 tgcgttaccc tccctactt cttcacgggt cgccggcgat tctcgccgat taccgacatg 840
 122 aacaagctcg gcgacccctt cgaccaggac agcaagtcg cgaacccgaa ccggctggag 900
 123 acgttccctcg acaaccacga tcgggccccgg ttccctcacct gggccgatga caactatcg 960
 124 cggctcgct caggactgac gttccctcta acctcccccgg gctcgccgt gatctactac 1020
 125 ggcaccggcaggc aggccgacca cggcaacggc aaccctacg agtaccgat cgccgacaa 1080
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 128 tggccgaca cctccgtcta cgggttctcg cgacgcgtcg acagcacggg tgccgaggcg 1260
 129 atgaccttct cgtcgaaactc gtggacgacg cagacgcgca cgggtccgat ggcgccc 1320
 130 agctcgatca cggcggtac gacgctgacg aacctcatga acacggcgat cacggtgacc 1380
 131 gtgaccggccg ggggtgtcac gggaaagcag atcaccgtct ccctcgccgat gacgagagc 1440
 132 aaggctatcg cgcggccac cccggatcg gcatacagcc cggacggcgat caacaccacg 1500
 133 aagatcccgatcg tgcactacaa cgtggccctc gggcacagca tcgacatccg cggcgacg 1560
 134 tacccttca cctggaccc cggccgaggc ggcgcaacg tcgacatccg cgtctgggag 1620
 135 ttccgagggtcg agccatccc cgacgggtcg accttccatcg tcaagccctt gatcgacg 1680
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 137 cccaccc
 139 <210> SEQ ID NO: 4
 140 <211> LENGTH: 9
 141 <212> TYPE: PRT
 142 <213> ORGANISM: Arthrobacter globiformis
 144 <400> SEQUENCE: 4
 145 His Ile Gln Arg Leu Thr Ala Ile Lys
 146 1 5
 148 <210> SEQ ID NO: 5
 149 <211> LENGTH: 13
 150 <212> TYPE: PRT
 151 <213> ORGANISM: Arthrobacter globiformis
 153 <400> SEQUENCE: 5
 154 Asp Met Glu Ser Phe Asp Gln Asn Ser Asn Leu Tyr Lys

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PATENT APPLICATION: US/10/569,959

DATE: 11/30/2006
TIME: 13:29:16

Input Set : N:\efs\11_30_06\10569959_efs\pto.da.txt
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157 <210> SEQ ID NO: 6
158 <211> LENGTH: 10
159 <212> TYPE: PRT
160 <213> ORGANISM: Arthrobacter globiformis
162 <400> SEQUENCE: 6
163 Leu Gly Asp Leu Phe Asp Gln Asp Ser Lys
164 1 5 10
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 27
168 <212> TYPE: PRT
169 <213> ORGANISM: Arthrobacter globiformis
171 <400> SEQUENCE: 7
172 Met Ile Leu Asp Val Val Pro Asn His Thr Ala Asp Tyr Leu Ala Gly
173 1 5 10 15
174 Thr Ser Thr Thr Tyr Ser Pro Ser Thr Tyr Lys
175 20 25
177 <210> SEQ ID NO: 8
178 <211> LENGTH: 20
179 <212> TYPE: PRT
180 <213> ORGANISM: Arthrobacter globiformis
182 <400> SEQUENCE: 8
183 Asp Trp Val Asp Met Gly Phe Asp Gly Ile Arg Val Asp Ala Ala Arg
184 1 5 10 15
185 Ser Val Pro Lys
186 20
188 <210> SEQ ID NO: 9
189 <211> LENGTH: 30
190 <212> TYPE: PRT
191 <213> ORGANISM: Arthrobacter globiformis
193 <400> SEQUENCE: 9
194 Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp Asn His Asp Arg
195 1 5 10 15
196 Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln Arg Leu
197 20 25 30
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 4467
201 <212> TYPE: DNA
202 <213> ORGANISM: Arthrobacter globiformis
204 <400> SEQUENCE: 10
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206 ctggcgaccg cagccggcga ggcacctctc ctccgcccgg ccgacctcggt ctacctcgcc 120
207 gtcgatctcg cgcagacgac ggagggagaa cggtcgcagc gggaggcgct cgggctcgct 180
208 gtcgtcgagc agaacgctct cgtcgccgat cctcgccgag ctgctcgac cgcacgagcc 240
209 cacctcgccc caggaccgtt catcgtgcac ctggacgtcg atgtgctgga cttcctcgac 300
210 gcaccccttg ccgagaacgt gaacggccga aacagcgggc cgaccgtcga gcagctcgcc 360
211 gtcgcactcg ccgagcttct gcagcatccg gactgctggg cgatgtccat cggccaggtg 420
212 gtccccgcgc acgcggcggc cgacccgacc tccatccgc ggctcatcg 480
213 gtgagctcca cgtagccgga cgtcgctcct ggagcggagc cgctccggca ggaacggcgt 540

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215	gcggcagcgt	gagccgcccac	cgaccagatc	tcatgcattt	ggacgaactt	cgccgtccaa	660										
216	ttctctccgc	gcctcaagca	ggtatacatc	gctcgAACgc	gtcttcactg	gcctgacgg	720										
217	ccgcgatcac	gtcgtgcagt	gaagcatcct	gccgcgaagg	gtcttgatgc	gcatgcagta	780										
218	cgggagtcga	atcaacttca	cgggcacggc	cgggtcagt	acttgacaaa	acgcatttat	840										
219	acatgttgca	tcgatccagt	aaaccgtgca	gctcgccgac	cgatgcgcac	ccgacaaacga	900										
220	agtcaggaga	gagtc	atg	aga	acg	aca	951										
221																	
	Met	Arg	Thr	Thr	Val	Arg	Thr										
						Ala	Arg										
222	1	5				Val	Ser										
						Ala											
224	cgt	acg	ggc	ctc	gcg	atg	999										
225	Arg	Thr	Gly	Leu	Ala	Met	Gly										
						Ala	Ala										
226	15			20			25										
228	ctc	acc	tgg	ggc	acc	ggc	ccc	gca	ccc	gca	gct	gac	ccc	acc	acg	999	
229	Leu	Thr	Trp	Gly	Thr	Gly	Pro	Ala	Pro	Ala	Ser	Ala	Asp	Pro	Thr	Thr	
230	30				35												
232	tcg	ccc	ggc	ccg	ctg	gcc	gag	ggc	gac	gtg	atc	tac	cag	gtg	ctc	gtc	1047
233	Ser	Pro	Gly	Pro	Leu	Ala	Glu	Gly	Asp	Val	Ile	Tyr	Gln	Val	Leu	Val	
234	45				50												
236	gac	ogg	ttc	gaa	gac	ggc	gac	ccc	acc	aac	gac	cag	ggc	gac	gga		1143
237	Asp	Arg	Phe	Glu	Asp	Gly	Asp	Pro	Thr	Asn	Asn	Asp	Gln	Gly	Asp	Gly	
238	65				70												
240	gag	tac	gat	ccg	tcc	gac	ctc	ggt	ttc	tac	cac	ggc	ggc	gac	tgg	gtc	1191
241	Glu	Tyr	Asp	Pro	Ser	Asp	Leu	Gly	Phe	Tyr	His	Gly	Gly	Asp	Trp	Ala	
242	80				85												
244	ggc	ctg	acg	gac	cg	ctc	gac	tac	atc	gcc	gat	ctg	ggt	gtg	acg	gct	1239
245	Gly	Leu	Thr	Asp	Arg	Leu	Asp	Tyr	Ile	Ala	Asp	Leu	Gly	Val	Thr	Ala	
246	95				100												
248	atc	tgg	ctc	tcg	ccc	gtc	tcc	gag	cag	cag	ccg	ctc	tcg	cg	gac	ggg	1287
249	Ile	Trp	Leu	Ser	Pro	Val	Ser	Glu	Gln	Gln	Pro	Leu	Ser	Arg	Asp	Gly	
250	110				115												
252	ctg	gag	gcc	agc	tac	cac	ggc	tac	ttc	act	cg	gac	ttc	gc	ac	ccg	1335
253	Leu	Glu	Ala	Ser	Tyr	His	Gly	Tyr	Phe	Thr	Arg	Asp	Phe	Ala	Thr	Pro	
254	125				130												
256	aac	gag	cat	ttc	ggc	gac	cga	gcc	gag	ctg	cag	ctg	atc	gac	acg	1383	
257	Asn	Glu	His	Phe	Gly	Asp	Arg	Ala	Glu	Leu	Gln	Glu	Leu	Ile	Asp	Thr	
258	145				150												
260	gcg	cac	gat	ctc	gga	ctc	aag	atg	atc	ctc	gac	gtc	gtg	ccg	aac	cac	1431
261	Ala	His	Asp	Leu	Gly	Leu	Lys	Met	Ile	Leu	Asp	Val	Val	Pro	Asn	His	
262	160				165												
264	acg	gcc	gac	tac	ctc	cg	ggc	aca	tcg	ac	acc	tat	tcg	ccg	agc	acc	1479
265	Thr	Ala	Asp	Tyr	Leu	Ala	Gly	Thr	Ser	Thr	Thr	Tyr	Ser	Pro	Ser	Thr	
266	175				180												
268	tac	aag	ccg	cg	agt	ccg	ctc	gat	gac	g	cg	tcg	tac	ttc	cat	cc	1527
269	Tyr	Lys	Pro	Ala	Ser	Pro	Leu	Asp	Asp	Ala	Ser	Tyr	Phe	His	His	Ala	
270	190				195												
272	ggc	gac	tgc	ctg	ttc	aac	ggg	ctc	gag	ac	cc	cag	atc	gag	aa	1575	
273	Gly	Asp	Cys	Leu	Phe	Asn	Gly	Leu	Glu	Thr	Gln	Thr	Gln	Ile	Glu	Asn	
274	205				210												
276	tgc	gac	ctc	ggc	ggg	ctc	gac	gac	ctc	gat	cag	tcg	aac	ccg	gtc	gtc	1623

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/569,959

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date